

CB #7

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,459

DATE: 09/13/2001

TIME: 17:32:29

Input Set : A:\ES.txt

Output Set: N:\CRF3\09132001\I807459.raw

3 <110> APPLICANT: IKADAI, Hiromi et al.
 5 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN FROM MEZORITE OF BABESIA CABALLI,
 RECOMBINANT

6 PROTEIN OBTAINED WITH SAID GENE AND USE THEREOF

8 <130> FILE REFERENCE: 0020-4843P

10 <140> CURRENT APPLICATION NUMBER: 09/807,459

11 <141> CURRENT FILING DATE: 2001-04-13

13 <160> NUMBER OF SEQ ID NOS: 2

15 <170> SOFTWARE: PatentIn version 3.0

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 1828

19 <212> TYPE: DNA

20 <213> ORGANISM: Babesia caballi

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (39)..(1412)

26 <400> SEQUENCE: 1

27 gtgccctggc cgcttcgccac aacagccgtg tttccatc atg gct ccc agc gac tct 56
 28 Met Ala Pro Ser Asp Ser
 29 1 5
 31 gtg ggc gac gtg act aag acc tta ttg gct gcc agc gaa agt gtg gac 104
 32 Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp
 33 10 15 20
 35 tca gct gcc aat gcc tat atg atc aac agt gac atg agc gat tac ttg 152
 36 Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu
 37 25 30 35
 39 tcg gct gtg tct gac aac ttc gcc gag cgc att tgc agt cag gtc cct 200
 40 Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro
 41 40 45 50
 43 aag ggg agt aac tgc agt gct tcc gtt agc gca tac atg agt cgc tgc 248
 44 Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys
 45 55 60 65 70
 47 gct aaa cag gac tgc ctg act ctc caa agt ctt aag tac cct ctt gag 296
 48 Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu
 49 75 80 85
 51 gct aag tac caa ccg ctg acc ctt cct gac ccc tac cag ttg gag gcc 344
 52 Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala
 53 90 95 100
 55 gca ttt ata ctc ttc aag gag agt gac gct aat ccg gcc aat agc act 392
 56 Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr
 57 105 110 115
 59 gag aag cgc ttc tgg atg cgt ttc aga agg ggc aag aac cac agt tac 440
 60 Glu Lys Arg Phe Trp Met Arg Phe Arg Arg Gly Lys Asn His Ser Tyr
 61 120 125 130
 63 ttc cac gac tta gtc ttc aat ctg ctg gag aag aac gtg act cgc gac 488
 64 Phe His Asp Leu Val Phe Asn Leu Leu Glu Lys Asn Val Thr Arg Asp
 65 135 140 145 150
 67 gcg gat gct act gac att gag aac ttt gcg tcc agg tac ctg tac atg 536

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68 Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala Ser Arg Tyr Leu Tyr Met
69          155          160          165
71 gcc acg ctt tac tac aag acg tac acg aat gtt gat gag ttc ggt gct      584
72 Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn Val Asp Glu Phe Gly Ala
73          170          175          180
75 agc ttc ttt aac aag ttg tct ttc act act ggg ttg ttc ggc tgg ggc      632
76 Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr Gly Leu Phe Gly Trp Gly
77          185          190          195
79 atc aag agg gca ctt aag cag att att cgc tct aac ctg ccc ctt gac      680
80 Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg Ser Asn Leu Pro Leu Asp
81          200          205          210
83 atc ggg aca gaa cac agc gtc agt cgc ctg cag cac att acg agc agt      728
84 Ile Gly Thr Glu His Ser Val Ser Arg Leu Gln His Ile Thr Ser Ser
85 215          220          225          230
87 tac aag gat tac atg gat acg cag att cct gca ctg ccc aag ttt gcg      776
88 Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro Ala Leu Pro Lys Phe Ala
89          235          240          245
91 aag cgt ttc tcc ctt atg gta gtg cag agg ctg ctg gcc acc gtg gct      824
92 Lys Arg Phe Ser Leu Met Val Val Gln Arg Leu Leu Ala Thr Val Ala
93          250          255          260
95 ggt tac gtc gac acc ccg tgg tat aag aag tgg tac atg aag ctg aag      872
96 Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys Trp Tyr Met Lys Leu Lys
97          265          270          275
99 aac ttt atg gtg aac agg gtg ttc att cct aca aag aag ttc ttc aat      920
100 Asn Phe Met Val Asn Arg Val Phe Ile Pro Thr Lys Lys Phe Phe Asn
101          280          285          290
103 aag gaa att cgt gag cct agt aag gca tta aaa gaa aag gtg tca acc      968
104 Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu Lys Glu Lys Val Ser Thr
105 295          300          305          310
107 gac acc aag gat tta ttc gag aac aaa att ggg cag ggt act gtg gac      1016
108 Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp
109          315          320          325
111 ttc ttc aat aag gaa att cgt gac cct agt aag gca tta aaa gaa aaa      1064
112 Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Lys Glu Lys
113          330          335          340
115 gtg tca aac gac gcc aag gat tta ttc gag aac aaa att ggg cag ggt      1112
116 Val Ser Asn Asp Ala Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly
117          345          350          355
119 act gtg gac ttc atc aat aac gaa att cgt gac cct agt aag gca tta      1160
120 Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser Lys Ala Leu
121          360          365          370
123 ata aga aaa gtg tca acg ggg gcc gag gat tta ttc gag aac aaa att      1208
124 Ile Arg Lys Val Ser Thr Gly Ala Glu Asp Leu Phe Glu Asn Lys Ile
125 375          380          385          390
127 ggg cag ggt act gtg gac ttc atc aat aac gaa att cgt gac cct agt      1256
128 Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser
129          395          400          405
131 aag gca tta ata aga aaa gtg tac acc gag gcc gat gat tta ttc gag      1304
132 Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu Ala Asp Asp Leu Phe Glu

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133          410          415          420
135 aac aaa att ggg cag ggt act gtg gac ttc atc aat aag gaa att cgt      1352
136 Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Lys Glu Ile Arg
137          425          430          435
139 gac cct agt aag gca tta ata aga aaa gtg tct acc gag gcc gat aat      1400
140 Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Glu Ala Asp Asn
141          440          445          450
143 tta ttg gag aaa taggttgaga agcccctgag gaagcaccgc aagggcaacg      1452
144 Leu Leu Glu Lys
145 455
147 ttagtgacag cggggaatct gaggaaatct cggctgtggg tgaatctttg gaatccgaca      1512
149 acgaaatgaa gaccacaggag tcaatgaact cggagagtgc ttctaccgaa ctcccttctg      1572
151 aggagtcgca ggaagagtgc gctgctatgg ttattcagca gccaccctg gagggagcca      1632
153 gccagatgcg attgcctgct gaagaagaca gctcagagtt gcaggaaacc tccgacaact      1692
155 atgaagcctc tctctagtca cctttgacgt ccatcgcact gctcggagaa tataaaacgc      1752
157 attgctcggg tgcactctag ttgttaacaa tgcacaatct aatgttatag ttgttttgaa      1812
159 aaaaaaaaaa aaaaaa      1828
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 458
164 <212> TYPE: PRT
165 <213> ORGANISM: Babesia caballi
167 <400> SEQUENCE: 2
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170 1          5          10          15
173 Ala Ser Glu Ser Val Asp Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser
174          20          25          30
177 Asp Met Ser Asp Tyr Leu Ser Ala Val Ser Asp Asn Phe Ala Glu Arg
178          35          40          45
181 Ile Cys Ser Gln Val Pro Lys Gly Ser Asn Cys Ser Ala Ser Val Ser
182          50          55          60
185 Ala Tyr Met Ser Arg Cys Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser
186 65          70          75          80
189 Leu Lys Tyr Pro Leu Glu Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp
190          85          90          95
193 Pro Tyr Gln Leu Glu Ala Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala
194          100          105          110
197 Asn Pro Ala Asn Ser Thr Glu Lys Arg Phe Trp Met Arg Phe Arg Arg
198          115          120          125
201 Gly Lys Asn His Ser Tyr Phe His Asp Leu Val Phe Asn Leu Leu Glu
202          130          135          140
205 Lys Asn Val Thr Arg Asp Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala
206 145          150          155          160
209 Ser Arg Tyr Leu Tyr Met Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn
210          165          170          175
213 Val Asp Glu Phe Gly Ala Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr
214          180          185          190
217 Gly Leu Phe Gly Trp Gly Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg
218          195          200          205
221 Ser Asn Leu Pro Leu Asp Ile Gly Thr Glu His Ser Val Ser Arg Leu

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222      210      215      220
225 Gln His Ile Thr Ser Ser Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro
226 225      230      235      240
229 Ala Leu Pro Lys Phe Ala Lys Arg Phe Ser Leu Met Val Val Gln Arg
230      245      250      255
233 Leu Leu Ala Thr Val Ala Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys
234      260      265      270
237 Trp Tyr Met Lys Leu Lys Asn Phe Met Val Asn Arg Val Phe Ile Pro
238      275      280      285
241 Thr Lys Lys Phe Phe Asn Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu
242      290      295      300
245 Lys Glu Lys Val Ser Thr Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile
246 305      310      315      320
249 Gly Gln Gly Thr Val Asp Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser
250      325      330      335
253 Lys Ala Leu Lys Glu Lys Val Ser Asn Asp Ala Lys Asp Leu Phe Glu
254      340      345      350
257 Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg
258      355      360      365
261 Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Gly Ala Glu Asp
262      370      375      380
265 Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn
266 385      390      395      400
269 Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu
270      405      410      415
273 Ala Asp Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe
274      420      425      430
277 Ile Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val
278      435      440      445
281 Ser Thr Glu Ala Asp Asn Leu Leu Glu Lys
282      450      455

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VERIFICATION SUMMARY

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